

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/806,930A
Source: TFW/6
Date Processed by STIC: 3-28-05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 03/28/2005

PATENT APPLICATION: US/10/806,930A

TIME: 11:23:29

Input Set : D:\Seqlist.txt

Output Set: N:\CRF4\03282005\J806930A.raw

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4 <110> APPLICANT: Lukyanov, Sergey
6 <120> TITLE OF INVENTION: Nucleic Acids Encoding Linked
7   Chromo/Fluorescent Domains and Methods for Using the Same
10 <130> FILE REFERENCE: CLON-094
12 <140> CURRENT APPLICATION NUMBER: us 10/806,930A
13 <141> CURRENT FILING DATE: 2004-03-22
15 <150> PRIOR APPLICATION NUMBER: 09/976,673
16 <151> PRIOR FILING DATE: 2001-10-12
18 <150> PRIOR APPLICATION NUMBER: 60/356,225
19 <151> PRIOR FILING DATE: 2002-02-11
21 <150> PRIOR APPLICATION NUMBER: 60/383,336
22 <151> PRIOR FILING DATE: 2002-05-22
24 <150> PRIOR APPLICATION NUMBER: PCT/US02/32560
25 <151> PRIOR FILING DATE: 2002-10-10
27 <160> NUMBER OF SEQ ID NOS: 13
29 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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32 <211> LENGTH: 1396
33 <212> TYPE: DNA
34 <213> ORGANISM: Anthozoa
36 <400> SEQUENCE: 1
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38 ggagggcacc gtgaacggcc actacttcaa gtgcgagggc gagggcgacg gcaacccctt 120
39 cgccggcacc cagagcatgc ggatccacgt gaccgagggc gccccctgc ccttcgcctt 180
40 cgacatcctg gccccctgct gcgagtacgg cagcaggacc ttctgtgcacc acaccgccga 240
41 gatccccgac ttcttcaagc agagcttccc cgagggttcc acctgggaga gaaccaccac 300
42 ctacgaggac ggcggcaccc tgaccgcccc ccaggacacc agcctggagg gcaactgcct 360
43 gatctacaag gtgaaggtgc tgggcaccaa ctccccgcc gacggccccg tgatgaagaa 420
44 caagagcggc ggctgggagc ccagcaccga ggtggtgtac cccgagaaac gcgtgctgtg 480
45 cgcccggaac gtgatggccc tgaaggtggg cgaccggcgg ctgatctgcc accactacac 540
46 cagctaccgg agcaagaagg ccgtgcgggc cctgaccatg cccggcttcc acttcaccga 600
47 catccggctg cagatgctgc ggaaggagaa ggacgagtag ttcgagctgt acgaggccag 660
48 cgtggcccgg tacagcgacc tgcccagaaa ggccaacaga tctcccggga tggtagcgcg 720
49 cctgctgaag gagagcatgc gcatcaagat gtacatggag ggcaccgtga acggccacta 780
50 cttcaagtgc gagggcgagg gcgacggcaa ccccttcgcc ggcaccaga gcatgcggat 840
51 ccacgtgacc gagggcgccc ccctgcccct cgccctcgac atcctggccc cctgctgcga 900
52 gtacggcagc aggaccttcg tgcaccacac cgccgagatc cccgacttct tcaagcagag 960
53 cttccccgag ggcttcacct gggagagaac caccacctac gaggacggcg gcatcctgac 1020
54 cgcccaccag gacaccagcc tggagggcaa ctgcctgatc tacaaggtga aggtgctggg 1080
55 caccaacttc cccgccgacg gccccgtgat gaagaacaag agcggcggct gggagcccag 1140
56 caccgaggtg gtgtaccccg agaacggcgt gctgtgcggc cggaacgtga tggccctgaa 1200
57 ggtgggcgac cggcggctga tctgcccacca ctaccagac taccggagca agaaggccgt 1260
58 gcgggcctg accatgcccc gcttccactt caccgacatc cggctgcaga tgctgcggaa 1320

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59 ggagaaggac gactacttcg agctgtacga ggccagcgtg gcccggtaca gcgacctgcc 1380
60 cgagaaggcc aactga                                     1396
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63 <211> LENGTH: 460
64 <212> TYPE: PRT
65 <213> ORGANISM: Anthozoa
67 <400> SEQUENCE: 2
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70 Glu Gly Thr Val Asn Gly His Tyr Phe Lys Cys Glu Gly Glu Gly Asp
71 20 25 30
72 Gly Asn Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu
73 35 40 45
74 Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu
75 50 55 60
76 Tyr Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe
77 65 70 75 80
78 Phe Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr
79 85 90 95
80 Tyr Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu
81 100 105 110
82 Gly Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro
83 115 120 125
84 Ala Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser
85 130 135 140
86 Thr Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val
87 145 150 155 160
88 Met Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr
89 165 170 175
90 Ser Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe
91 180 185 190
92 His Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Glu Lys Asp Glu
93 195 200 205
94 Tyr Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro
95 210 215 220
96 Glu Lys Ala Asn Arg Ser Pro Gly Met Val Ser Gly Leu Leu Lys Glu
97 225 230 235 240
98 Ser Met Arg Ile Lys Met Tyr Met Glu Gly Thr Val Asn Gly His Tyr
99 245 250 255
100 Phe Lys Cys Glu Gly Glu Gly Asp Gly Asn Pro Phe Ala Gly Thr Gln
101 260 265 270
102 Ser Met Arg Ile His Val Thr Glu Gly Ala Pro Leu Pro Phe Ala Phe
103 275 280 285
104 Asp Ile Leu Ala Pro Cys Cys Glu Tyr Gly Ser Arg Thr Phe Val His
105 290 295 300
106 His Thr Ala Glu Ile Pro Asp Phe Phe Lys Gln Ser Phe Pro Glu Gly
107 305 310 315 320
108 Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu Asp Gly Gly Ile Leu Thr
109 325 330 335

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110 Ala His Gln Asp Thr Ser Leu Glu Gly Asn Cys Leu Ile Tyr Lys Val
111           340           345           350
112 Lys Val Leu Gly Thr Asn Phe Pro Ala Asp Gly Pro Val Met Lys Asn
113           355           360           365
114 Lys Ser Gly Gly Trp Glu Pro Ser Thr Glu Val Val Tyr Pro Glu Asn
115           370           375           380
116 Gly Val Leu Cys Gly Arg Asn Val Met Ala Leu Lys Val Gly Asp Arg
117 385           390           395           400
118 Arg Leu Ile Cys His His Tyr Thr Ser Tyr Arg Ser Lys Lys Ala Val
119           405           410           415
120 Arg Ala Leu Thr Met Pro Gly Phe His Phe Thr Asp Ile Arg Leu Gln
121           420           425           430
122 Met Leu Arg Lys Glu Lys Asp Glu Tyr Phe Glu Leu Tyr Glu Ala Ser
123           435           440           445
124 Val Ala Arg Tyr Ser Asp Leu Pro Glu Lys Ala Asn
125           450           455           460
128 <210> SEQ ID NO: 3
129 <211> LENGTH: 1424
130 <212> TYPE: DNA
131 <213> ORGANISM: Anthozoa
133 <400> SEQUENCE: 3
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135 ggagggcacc gtgaacggcc actacttcaa gtgcgagggc gagggcgacg gcaacccctt 120
136 cgccggcacc cagagcatgc ggatccacgt gaccgagggc gccccctgc ccttcgcctt 180
137 cgacatcctg gccccctgct gcgagtacgg cagcaggacc ttcgtgcacc acaccgccga 240
138 gatccccgac ttcttcaagc agagcttccc cgagggtctt acctgggaga gaaccaccac 300
139 ctacgaggac ggcggcatcc tgaccgcca ccaggacacc agcctggagg gcaactgcct 360
140 gatctacaag gtgaaggtgc tgggaccaa cttccccgcc gacggccccg tgatgaagaa 420
141 caagagcggc ggctgggagc ccagcaccga ggtggtgtac cccgagaacg gcgtgctgtg 480
142 cggccggaac gtgatggccc tgaaggtggg cgaccggcgg ctgatctgcc accactacac 540
143 cagctaccgg agcaagaagg ccgtgcgggc cctgaccatg cccggcttcc acttcaccga 600
144 catccggctg cagatgctgc ggaaggagaa ggacgagtac ttcgagctgt acgaggccag 660
145 cgtggccccg tacagcgacc tgcccgagaa ggccaacaga tctccccgga tggtgagcgg 720
146 cctgctgaag gagagcatgc gcatcaagat gtacatggag ggcaccgtga acggccacta 780
147 cttcaagtgc gagggcgagg gcgacggcaa ccccttcgcc ggcaccaga gcatgcggat 840
148 ccacgtgacc gagggcgccc ccctgccctt cgccttcgac atcctggccc cctgctgcga 900
149 gtacggcagc aggaccttcg tgcaccacac cgccgagatc cccgacttct tcaagcagag 960
150 cttccccgag ggcttcacct gggagagaa caccacctac gaggacggcg gcatcctgac 1020
151 cgccaccag gacaccagcc tggagggcaa ctgcctgatc tacaaggtga aggtgctggg 1080
152 caccaacttc cccgccgacg gccccgtgat gaagaacaag agcggcggtt gggagcccag 1140
153 caccgaggtg gtgtaccccc agaacggcgt gctgtgcggc cggaacgtga tggccctgaa 1200
154 ggtgggcgac cggcggtga tctgccacca ctacaccagc taccggagca agaaggccgt 1260
155 gcgggccctg accatgcccg gcttccactt caccgacatc cggtgcaga tgctgcggaa 1320
156 ggagaaggac gagtacttcg agctgtacga ggccagcgtg gcccgtaca gcgacctgcc 1380
157 cgagaaggcc aacagaactc gagctatgga tgatgatatc gccg 1424
159 <210> SEQ ID NO: 4
160 <211> LENGTH: 470
161 <212> TYPE: PRT
162 <213> ORGANISM: Anthozoa

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164 <400> SEQUENCE: 4

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165 Met Val Ser Gly Leu Leu Lys Glu Ser Met Arg Ile Lys Met Tyr Met
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167 Glu Gly Thr Val Asn Gly His Tyr Phe Lys Cys Glu Gly Glu Gly Asp
168 20 25 30
169 Gly Asn Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu
170 35 40 45
171 Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu
172 50 55 60
173 Tyr Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe
174 65 70 75 80
175 Phe Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr
176 85 90 95
177 Tyr Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu
178 100 105 110
179 Gly Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro
180 115 120 125
181 Ala Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser
182 130 135 140
183 Thr Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val
184 145 150 155 160
185 Met Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr
186 165 170 175
187 Ser Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe
188 180 185 190
189 His Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Glu Lys Asp Glu
190 195 200 205
191 Tyr Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro
192 210 215 220
193 Glu Lys Ala Asn Arg Ser Pro Gly Met Val Ser Gly Leu Leu Lys Glu
194 225 230 235 240
195 Ser Met Arg Ile Lys Met Tyr Met Glu Gly Thr Val Asn Gly His Tyr
196 245 250 255
197 Phe Lys Cys Glu Gly Glu Gly Asp Gly Asn Pro Phe Ala Gly Thr Gln
198 260 265 270
199 Ser Met Arg Ile His Val Thr Glu Gly Ala Pro Leu Pro Phe Ala Phe
200 275 280 285
201 Asp Ile Leu Ala Pro Cys Cys Glu Tyr Gly Ser Arg Thr Phe Val His
202 290 295 300
203 His Thr Ala Glu Ile Pro Asp Phe Phe Lys Gln Ser Phe Pro Glu Gly
204 305 310 315 320
205 Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu Asp Gly Gly Ile Leu Thr
206 325 330 335
207 Ala His Gln Asp Thr Ser Leu Glu Gly Asn Cys Leu Ile Tyr Lys Val
208 340 345 350
209 Lys Val Leu Gly Thr Asn Phe Pro Ala Asp Gly Pro Val Met Lys Asn
210 355 360 365
211 Lys Ser Gly Gly Trp Glu Pro Ser Thr Glu Val Val Tyr Pro Glu Asn
212 370 375 380

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213 Gly Val Leu Cys Gly Arg Asn Val Met Ala Leu Lys Val Gly Asp Arg
214 385                               390                               395                               400
215 Arg Leu Ile Cys His His Tyr Thr Ser Tyr Arg Ser Lys Lys Ala Val
216                               405                               410                               415
217 Arg Ala Leu Thr Met Pro Gly Phe His Phe Thr Asp Ile Arg Leu Gln
218                               420                               425                               430
219 Met Leu Arg Lys Glu Lys Asp Glu Tyr Phe Glu Leu Tyr Glu Ala Ser
220                               435                               440                               445
221 Val Ala Arg Tyr Ser Asp Leu Pro Glu Lys Ala Asn Arg Thr Arg Ala
222                               450                               455                               460
223 Met Asp Asp Asp Ile Ala
224 465                               470
227 <210> SEQ ID NO: 5
228 <211> LENGTH: 1376
229 <212> TYPE: DNA
230 <213> ORGANISM: Anthozoa
232 <400> SEQUENCE: 5
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234 ggccattatt tcaagtgtga aggagaggga gacggcaacc catttgcagg tacgcagagc 120
235 atgaggattc atgtcaccga aggggctcca ttaccatttg ccttcgacat tttggcaccg 180
236 tgttgtgagt acggcagcag gacctttgtc caccatacgg cagagattcc cgatttcttc 240
237 aagcagtcctt tccctgaagg ctttacttgg gaaagaacca caacctatga agatggaggc 300
238 attcctactg ctcctcagga cacaagcctg gaggggaact gccttatata caaggtgaaa 360
239 gtccatggta ccaattttcc tgctgatggc cccgtgatga agaacaaatc aggaggatgg 420
240 gagccaagca ctgaggtggg ttatccagag aatgggtgtcc tgtgtggacg taatgtgatg 480
241 gcccttaaag tcggtgatcg tcatttgatc tgccatcact atacttctta cagggtccaag 540
242 aaagcagtcg gtgccttgac aatgccagga tttcatttta cagacatccg ccttcagatg 600
243 ctgaggaaaa agaaaagcga gtactttgaa ctgtacgaag catctgtggc taggtacagt 660
244 gatcttcctg aaaaagcaaa agatctcccg ggatgtctgg tttgttgaaa gaaagtatgc 720
245 gcatcaagat gtacatggaa ggcacgggta atggccatta tttcaagtgt gaaggagagg 780
246 gagacggcaa cccatttgca ggtacgcaga gcatgaggat tcatgtcacc gaaggggctc 840
247 cattaccatt tgccttcgac attttggcac cgtgttgtga gtacggcagc aggacctttg 900
248 tccaccatac ggcagagatt cccgatttct tcaagcagtc tttccctgaa ggctttactt 960
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252 agaatgggtg cctgtgtgga cgtaaatgtga tggcccttaa agtcggtgat cgtcatttga 1200
253 tctgccatca ctatacttct tacaggtcca agaaagcagt ccgtgccttg acaatgccag 1260
254 gatttcattt tacagacatc cgccttcaga tgctgaggaa aaagaaagac gagtactttg 1320
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258 <211> LENGTH: 458
259 <212> TYPE: PRT
260 <213> ORGANISM: Anthozoa
262 <400> SEQUENCE: 6
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264 1 5 10 15
265 Gly Thr Val Asn Gly His Tyr Phe Lys Cys Glu Gly Glu Gly Asp Gly
266 20 25 30

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VERIFICATION SUMMARY

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